

# Package ‘`phylolm.hp`’

November 23, 2024

**Type** Package

**Title** Hierarchical Partitioning of R2 for Phylogenetic Linear Regression

**Version** 0.0-2

**Date** 2024-11-18

**Depends** R (>= 3.4.0),rr2,phylolm,ggplot2,vegan

**Maintainer** Jiangshan Lai <lai@njfu.edu.cn>

**Description** Conducts hierarchical partitioning to calculate individual contributions of phylogenetic tree and predictors (groups) towards total R2 for phylogenetic linear regression models.

**License** GPL

**Encoding** UTF-8

**URL** <https://github.com/laijiangshan/phylolm.hp>

**RoxygenNote** 7.3.1

**NeedsCompilation** no

**Author** Jiangshan Lai [aut, cre] (<<https://orcid.org/0000-0002-0279-8816>>),  
Gang Wang [aut]

**Repository** CRAN

**Date/Publication** 2024-11-23 14:40:02 UTC

## Contents

phyloglm.hp . . . . .	2
plot.phyloglmhp . . . . .	3
<b>Index</b>	<b>5</b>

---

phyloglm.hp	<i>Hierarchical Partitioning of R2 for Phylogenetic Generalized Linear Regression</i>
-------------	---

---

## Description

Hierarchical Partitioning of R2 for Phylogenetic Generalized Linear Regression

## Usage

```
phyloglm.hp(mod, iv = NULL, commonality = FALSE)
```

## Arguments

mod	Fitted phylolm or phyloglm model objects.
iv	optional the relative importance of predictor groups will be evaluated. The input for iv should be a list containing the names of each group of variables. The variable names must be the names of the predictor variables in mod.
commonality	Logical; If TRUE, the result of commonality analysis is shown, the default is FALSE.

## Details

This function conducts hierarchical partitioning to calculate the individual contributions of phylogenetic signal and each predictor towards total R2 from rr2 package for phylogenetic linear regression.

## Value

Total.R2	The R2 for the full model.
commonality.analysis	If commonality=TRUE, a matrix containing the value and percentage of all commonality ( $2^N - 1$ for N predictors or matrices).
Individual.R2	A matrix containing individual effects and percentage of individual effects for phylogenetic tree and each predictor

## Author(s)

Jiangshan Lai <lai@njfu.edu.cn>

## References

- Lai J.,Zhu W., Cui D.,Mao L.(2023)Extension of the glmm.hp package to Zero-Inflated generalized linear mixed models and multiple regression.Journal of Plant Ecology,16(6):rtad038<DOI:10.1093/jpe/rtad038>
- Lai J.,Zou Y., Zhang S.,Zhang X.,Mao L.(2022)glmm.hp: an R package for computing individual effect of predictors in generalized linear mixed models.Journal of Plant Ecology,15(6):1302-1307<DOI:10.1093/jpe/rtac096>

- Lai J., Zou Y., Zhang J., Peres-Neto P. (2022) Generalizing hierarchical and variation partitioning in multiple regression and canonical analyses using the rdacca.hp R package. *Methods in Ecology and Evolution*, 13(4):782-788 <DOI:10.1111/2041-210X.13800>
- Chevan, A. & Sutherland, M. (1991). Hierarchical partitioning. *American Statistician*, 45, 90-96. doi:10.1080/00031305.1991.10475776
- Nimon, K., Oswald, F.L. & Roberts, J.K. (2013). Yhat: Interpreting regression effects. R package version 2.0.0.
- Nimon, Ho, L. S. T. and Ane, C. 2014. "A linear-time algorithm for Gaussian and non-Gaussian trait evolution models". *Systematic Biology* 63(3):397-408.

## Examples

```

library(phyloilm)
library(rr2)
set.seed(231)
tre <- rcoal(60)
taxa <- sort(tre$tip.label)
b0 <- 0
b1 <- 0.3
b2 <- 0.5
b3 <- 0.4
x <- rTrait(n=1, phy=tre, model="lambda", parameters=list(ancestral.state=0, sigma2=15, lambda=0.9))
x2 <- rTrait(n=1, phy=tre, model="lambda",
parameters=list(ancestral.state=0, sigma2=10, lambda=0.9))
x3 <- rTrait(n=1, phy=tre, model="lambda",
parameters=list(ancestral.state=0, sigma2=13, lambda=0.9))
y <- b0 + b1 * x + b2 * x2 + b3*x3+ rTrait(n=1, phy=tre, model="lambda",
parameters=list(ancestral.state=0, sigma2=5, lambda=0.9))
dat <- data.frame(trait=y[taxa], pred=x[taxa], pred2=x2[taxa], pred3=x3[taxa])
fit <- phyloilm(trait ~ pred + pred2 + pred3, data=dat, phy=tre, model="lambda")
phyloglm.hp(fit, commonality=TRUE)
iv=list(env1="pred", env2=c("pred2", "pred3"))
phyloglm.hp(fit, iv)
set.seed(123456)
tre <- rtree(50)
x1 <- rTrait(n=1, phy=tre)
x2 <- rTrait(n=1, phy=tre)
x3 <- rTrait(n=1, phy=tre)
X <- cbind(rep(1, 50), x1, x2, x3)
y <- rbinTrait(n=1, phy=tre, beta=c(-1, 0.9, 0.9, 0.5), alpha=1, X=X)
dat <- data.frame(trait01=y, predictor1=x1, predictor2=x2, predictor3=x3)
fit <- phyloglm(trait01 ~ predictor1 + predictor2 + predictor3, phy=tre, data=dat)
phyloglm.hp(fit)
iv=list(env1="predictor1", env2=c("predictor2", "predictor3"))
phyloglm.hp(fit, iv)

```

**Description**

Plot for a `phyloglm.hp` object

**Usage**

```
## S3 method for class 'phyloglmhp'
plot(x, plot.perc = FALSE, commonality = FALSE, color = NULL, dig = 4, ...)
```

**Arguments**

<code>x</code>	A <code>phyloglm.hp</code> object.
<code>plot.perc</code>	Logical; if TRUE, the bar plot (based on ggplot2 package) of the percentage to individual effects of variables and phylogenetic signal towards total explained variation, the default is FALSE to show plot with original individual effects.
<code>commonality</code>	Logical; If TRUE, the result of commonality analysis is shown, the default is FALSE.
<code>color</code>	Color of variables.
<code>dig</code>	Integer; number of decimal places in Venn diagram.
<code>...</code>	unused

**Value**

a ggplot object

**Author(s)**

Jiangshan Lai <lai@njfu.edu.cn>

**Examples**

```
library(phyloilm)
library(rr2)
set.seed(123456)
tre <- rtree(50)
x1 <- rTrait(n=1, phy=tre)
x2 <- rTrait(n=1, phy=tre)
X <- cbind(rep(1, 50), x1, x2)
y <- rbinTrait(n=1, phy=tre, beta=c(-1, 0.8, 0.9), alpha=1, X=X)
dat <- data.frame(trait01=y, predictor1=x1, predictor2=x2)
fit <- phyloglm(trait01 ~ predictor1 + predictor2, phy=tre, data=dat)
plot(phyloglm.hp(fit, commonality=TRUE))
plot(phyloglm.hp(fit, commonality=TRUE), commonality=TRUE)
```

# Index

phyloglm.hp, [2](#), [3](#), [4](#)  
plot.phyloglmhp, [3](#)